

REMARKS

Pending Claims

Claims 1 and 50-74 are pending. Claims 62-74 are withdrawn pending rejoinder.

Restriction and Linking Claims

Applicants assert the elected product group and new product claim 1 is properly linked to claims that recite a method of using the product of claim 1, as well as to claims drawn to combinations/subcombinations that require all the limitations of the claimed product of claim 1. The claimed malt (malted kernels or grain) and wort (mashed malted grain) are each part of the plant or portion of claim 1. The claimed beverages are products produced using the claimed plant or plant portion of claim 1. Accordingly, the malt, wort, and beverage claims, each requiring all the limitations of claim 1, are linked to claim 1 as products produced from the claimed plant and/or as combinations and/or subcombinations permitted by MPEP section 809. Allowance of the product claims 1 and 50-59 and rejoinder of the linked claims 62-74 is respectfully requested.

Examiner Interviews

The Applicant's representative thanks Examiner Ibrahim for her kind assistance during the recent telephone interviews. The attached documents are copies of those submitted for discussion with the Examiner, and include, draft claims, sequence alignments, and listing of support in the specification for the claims. These documents are submitted for the prosecution record in this case, as requested by the Examiner.

Conclusion

In light of the forgoing Amendment and Remarks, Applicant's respectfully assert the claims are in condition for allowance. Early notice of such allowance is solicited.

The Examiner is invited to telephone the undersigned attorney for clarification of any of these remarks and/or to otherwise speed prosecution of this case.



Respectfully submitted,

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Dated: 18 October 2007

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Draft Claims, + Seq. Align attached for review + discussion.

Symnda Kieft
on behalf of D. Kettelberger

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M&G 12845.9USWO
Draft Claims

For Discussion Only

SEQUENCES:

1. The specification and claims recite four LOX-1 proteins of interest, wild-type (cv Barke and cv Neruda) and Mutants D112 and A618. Please note that the WT nucleic acid sequences (SEQ ID NO: 1 and 5) and amino acid sequences (SEQ ID NO: 3 and 7) of LOX-1 are identical between these two barley varieties. (see the sequence comparison (1)).
2. Two mutants are exemplified, each containing a single nucleic acid change. In mutant A618, the gene is mutated at position 2311 changing G to A (SEQ ID NO: 6). See the nucleic acid comparison (2) at page 5. In mutant D112, nucleic acid 3574 is changed from G to A (SEQ ID NO: 2). See the nucleic acid comparison at page 7.
3. The point mutation in the nucleic acid sequence causes a splice variant mutant protein in mutant A618 (SEQ ID NO: 8), truncating the LOX-1 protein sequence at amino acid 378 and retaining a few non LOX-1 amino acids. See the amino acid comparison (3) on the first page. For mutant D112, the point mutation creates a stop codon, resulting in truncation of the LOX-1 protein at amino acid 665 (SEQ ID NO: 4). See the amino acid comparison at page 2.
4. Thus the two barley lox-1 wild type nucleic acid sequences are identical; the two mutant nucleic acid sequences each differ from the WT only in one amino acid. The two barley LOX-1 wild type protein sequences are identical; one mutant LOX-1 sequence, A618, is truncated at **378** and contains 21 additional non-LOX-1 amino acids; the second mutant, D112 is truncated at amino acid **665**.
5. The LOX-1 protein contains a LOX-1 enzymatic domain corresponding to amino acids **520-862**.

Barley	Lox-1 Gene	LOX-1 Protein	LOX-1 AA
WT cv Barke	SEQ ID NO: 1	SEQ ID NO: 3	1-862
WT cv Neruda	SEQ ID NO: 5	SEQ ID NO: 7	1-862
Mut D112	SEQ ID NO: 2	SEQ ID NO: 4	1-665
Mut A618	SEQ ID NO: 6	SEQ ID NO: 8	1-378 + 21 non

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CLAIMS

1. In the proposed claim amendment, Claim 1 is amended to include the amino acids of the C-terminal enzymatic domain **520-862**, as you suggested. The WT barley sequence is identified as SEQ ID NO: 3 or 7. (Note the two barley sequences are identical, and reference to only one would suffice.) Support for this amendment is found, for example at page 26, beginning at line 12:

The term LOX-1 protein is meant to cover the full length LOX-1 protein of barley as set forth in [SEQ ID NO: 3] or [SEQ ID NO: 7] or a functional homologue thereof. The active site of LOX-1 is situated in the C-terminal part of LOX-1. In particular is the region spanning amino acid residues 520-862 or parts thereof relevant for LOX-1 activity. Accordingly, in one embodiment null-LOX-1 barley preferably comprises a gene encoding a mutant form of LOX-1 **lacking some or all of amino acids 520-862** of LOX-1. Said mutant LOX-1 may also lack other amino acid residues which are present in wild-type LOX-1.

2. New claim 50 recites truncation of LOX-1 at a position at or between amino acids **378 and 665**. The mutants demonstrated in the examples contain a LOX-1 protein truncated at position **665** (D112 in Example 10) and at position **378** (A618 in Example 11). Example 10 describes the truncated D112 LOX-1 protein as:

The stop-codon in the LOX-1 encoding gene of the mutant D112 is predicted to result in a C-terminal truncation of 197 amino acids of the corresponding protein.... the sequence of which is listed in [SEQ ID NO:4].

Subtracting the 197 aa truncation from the 892 aa of the LOX-1 protein results in a mutant protein of containing amino acids **1-665** of LOX-1. See also Figure 15, listing mutant D112 as having 665 amino acids; see also SEQ ID NO:4 having 665 amino acids.

Example 11 describes the mutation in A618 to be in the intron 3 donor site, and causing a splice error in intron 3 leading to a stop codon in the intron 3 after translation of 399 amino acids. The truncated translated protein (SEQ ID NO: 8) includes both LOX-1 amino acids and amino acids of the intron. Comparison of the mutated protein and wild type LOX-1 demonstrates that the mutant protein includes amino acids **1-378** plus 21 non-LOX 1 amino acids. ($378 + 21 = 399$).

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The specification further supports the truncation between 378 and 665. See, for example, page 30:

In one embodiment of the invention the barley plant comprises a gene encoding a mutant LOX-1, wherein said gene has a mutation in a splice site leading to mRNA encoding a protein consisting of amino acids **1 to 378** of [SEQ ID NO: 3] as well as an additional amino acid sequence not derived from LOX-1. Preferably, said mutant LOX-1 consists of the sequence as outlined in [SEQ ID NO: 8].

3. Proposed claim 51 recites amino acids **1-378**; Proposed claim 52 recites SEQ ID NO:4 (D112) or 8 (A618). Each of these claims is supported by the specification, for example, as described above.
4. Proposed claims 53 -55 are amended to recite mutations of the gene in terms of the mutated protein, as you requested. Support for the gene mutations is found, for example in Figure 15 and in Examples 10 and 11. Mutant A618 contains a nucleic acid point mutation at position **2311** and mutant D112 contains a point mutation at position **3574**. Each point mutation results in a stop codon and truncated LOX-1 protein. The mutated genes have the sequences of SEQ ID NOs: **2** (D112) and **6** (A618)
5. Proposed claim 56 recites the ATCC deposit numbers for the mutant plants. Support is found, for example at page 30, including progeny.
6. Proposed claims 57 and 58 recite plant portions as kernels and embryos. Support for these plant portions is found, for example, at page 63 and particularly in the Examples demonstrating use of barley kernels for preparing malt, wort, and beer.
7. Proposed claim 58 recites a test for screening mutant LOX-1 activity in the M3 or M4 generation plants. Support is found in Examples 1, 2, 3, and 17, for example.
8. Proposed claims 60 and 61 are method of screening claims that have been restricted (original claim 48 for example). These claim should be marked (New and Withdrawn).
9. Proposed claims 62-64 are restricted claims that are withdrawn and subject to rejoinder on indication of allowable subject matter.

What is claimed is:

1. (Amended) A barley plant, ~~or a part thereof,~~ or a portion of said plant, comprising
~~less than 5% of the LOX-1 activity of a wild-type barley plant~~
a mutated LOX-1 protein lacking all or a portion of the C-terminal LOX-1 enzymatic domain corresponding to amino acids 520 to 862 of wild type barley LOX-1 (SEQ ID NO: 3 or 7), wherein said plant exhibits null LOX-1 activity.
- 2-49. (Cancelled)
50. (New) The barley plant or portion according to claim 1, wherein said mutated LOX-1 protein is truncated at or between amino acids 378 and 665 of wild-type barley LOX-1.
51. (New) The barley plant or portion according to claim 1, wherein said mutated LOX-1 protein consists essentially of amino acids 1-378 of wild-type barley LOX-1 (SEQ ID NO: 3 or 7).
52. (New) The barley plant or portion according to claim 1, wherein said mutated LOX-1 protein has the amino acid sequence of SEQ ID NO. 4 or 8.
53. (New) The barley plant or portion according to claim 1, wherein said mutated LOX-1 protein is encoded by a gene that comprises a premature stop codon at or between nucleotides 2311 and 3574 of wild-type genomic barley lox-1 (SEQ ID NO: 1 or 5).
54. (New) The barley plant or portion according to claim 1, wherein said mutated LOX-1 protein is encoded by a gene that comprises a stop codon at nucleotides 3572-3574 of wild-type genomic barley lox-1 (SEQ ID NO: 1 or 5).
55. (New) The barley plant or portion according to claim 1, wherein said mutated LOX-1 protein is encoded by a gene that comprises the nucleic acid sequence of SEQ ID NO: 2 or 6.
56. (New) The barley plant or portion according to claim 1, wherein said plant has ATCC accession No. PTA-5847 or PTA-5584, or is a progeny plant thereof.
57. (New) The barley plant or portion according to claim 1, wherein said portion comprises a kernel.
58. (New) The barley plant or portion according to claim 1, wherein said portion comprises an embryo.
59. (New) The barley plant or portion according to claim 1, wherein said LOX-1 activity is determined in homogenized embryo tissue of M3 or M4 plant kernels.

60. (New and **Withdrawn**) A method for selecting mutant barley plants having null LOX-1 activity, comprising:
 - a. breeding mutagenized barley plants or tissue obtained therefrom to produce generation Mx barley plants, where x is at least 2; and
 - b. selecting plants having null LOX-1 activity in kernel tissue of said generation Mx plants.
61. (New and **Withdrawn**) The method of claim 60, wherein said selecting is of generation M3 or M4 plants.
62. (New and Withdrawn) A **malt** composition comprising malted kernels of the plant of claim 1.
63. (New and Withdrawn) A **malt** composition comprising malted kernels of the plant of claim 54.
64. (New and Withdrawn) A **wort** composition comprising malted and mashed kernels of a plant of claim 1.
65. (New and Withdrawn) A **beverage** prepared from the plant or plant portion of claim 1, wherein the plant or portion is malted or unmalted.
66. (New and Withdrawn) A **beverage** prepared from the plant or plant portion of claim 54, wherein the plant or portion is malted or unmalted.
67. (New and Withdrawn) A **beverage** prepared from the plant or plant portion of claim 1, wherein the beverage is non-fermented or fermented.
68. (New and Withdrawn) A **beverage** prepared from the plant or plant portion of claim 1, wherein the beverage contains 9, 12, 13-trihydroxyoctadecanoic acid and 9, 10, 13-trihydroxyoctadecanoic acid in a ratio of no more than 1.8.
69. (New and Withdrawn) **Beer** prepared from the plant or plant portion of claim 1.
70. (New and Withdrawn) **Beer** prepared from the plant or plant portion of claim 54.
71. (New and Withdrawn) **Beer** prepared from kernels of the plant of claim 1.
72. (New and Withdrawn) **Beer** prepared from grain of the plant of claim 1.
73. (New and Withdrawn) **Beer** prepared from malted grain of the plant of claim 1.
74. (New and Withdrawn) **Beer** prepared from mashed malted grain of the plant of claim 1.

CLUSTAL W (1.8) multiple sequence alignment

LOI-1

Compare WT cv Barke vs Neruda
- identical -

WT
WT

SEQID3 Barke
SEQID7 Neruda

MLLGGLIDTLTGANKSARLKGTVVLMRKNVLDLNDFGATIIDGIGEFGLGKGVTCQLISST
MLLGGLIDTLTGANKSARLKGTVVLMRKNVLDLNDFGATIIDGIGEFGLGKGVTCQLISST

SEQID3
SEQID7
AVDQDNGGRGKVGAEAELEQWVTSPLSLTTGESKFGLTFDWEVEKLGVPGAIVVNNYHSS
AVDQDNGGRGKVGAEAELEQWVTSPLSLTTGESKFGLTFDWEVEKLGVPGAIVVNNYHSS

SEQID3
SEQID7
EFLKTTITLHDVPGRSGNLTFVANSWIYPAANYRYSRVFFANDTYLPSQMPAALKPYRDD
EFLKTTITLHDVPGRSGNLTFVANSWIYPAANYRYSRVFFANDTYLPSQMPAALKPYRDD

SEQID3
SEQID7
ELRNLRGDDQQGPYQEHDRIYRYDVYNDLGEGRPILGGNSDHPYPRRGRTERKPNASDPS
ELRNLRGDDQQGPYQEHDRIYRYDVYNDLGEGRPILGGNSDHPYPRRGRTERKPNASDPS

SEQID3
SEQID7
LESRLSLEQIYVPRDEKFGHLKTSDFLGYSIKAITQGILPAVRTYVDTPGGEFDSFQDI
LESRLSLEQIYVPRDEKFGHLKTSDFLGYSIKAITQGILPAVRTYVDTPGGEFDSFQDI

SEQID3
SEQID7
INLYEGGIKLPKVAALEELRKQFPLQLIKDLLPVGGDSLLKLPVPHIIQENKQAWRTDEE
INLYEGGIKLPKVAALEELRKQFPLQLIKDLLPVGGDSLLKLPVPHIIQENKQAWRTDEE

SEQID3
SEQID7
FAREVLAGVNPVMITRLTEFPKSSLDPSKFGDHTSTITAHEIEKNLEGLTVQQALESNR
FAREVLAGVNPVMITRLTEFPKSSLDPSKFGDHTSTITAHEIEKNLEGLTVQQALESNR

SEQID3
SEQID7
LYILDHHRFMPFLIDVNNLPGNFIYATRTLFFLRGDGRLTPLAIELSEPIIQGGLTTAK
LYILDHHRFMPFLIDVNNLPGNFIYATRTLFFLRGDGRLTPLAIELSEPIIQGGLTTAK

SEQID3
SEQID7
SKVYTPVPSGSVEGWVWELAKAYVAVNDSGWHQLVSHWLNTHAVMEPFVISTNRHLSVTH
SKVYTPVPSGSVEGWVWELAKAYVAVNDSGWHQLVSHWLNTHAVMEPFVISTNRHLSVTH

SEQID3
SEQID7
PVHKLLSPHYRDTMTINALARQTLINAGGIFEMTVFPGKFALGMSAVVYKDWKFTEQGLP
PVHKLLSPHYRDTMTINALARQTLINAGGIFEMTVFPGKFALGMSAVVYKDWKFTEQGLP

SEQID3
SEQID7
DDLKRGMAVEDPSSPYKVRLLVSDYPYAADGLAIWHAIEQYVSEYLAIYYPNDGVLQGD
DDLKRGMAVEDPSSPYKVRLLVSDYPYAADGLAIWHAIEQYVSEYLAIYYPNDGVLQGD

SEQID3
SEQID7
TEVQAWWKETREVGHGDLKDAPWWPKMQSVPELAKACTTIIWIGSALHAAVNFGQYPYAG
TEVQAWWKETREVGHGDLKDAPWWPKMQSVPELAKACTTIIWIGSALHAAVNFGQYPYAG

SEQID3
SEQID7
FLPNRPTVSRRRMPEPGTEEYAELEDPERAFIHTITSQIQTIIGVSLLEVLSKHSSDEL
FLPNRPTVSRRRMPEPGTEEYAELEDPERAFIHTITSQIQTIIGVSLLEVLSKHSSDEL

SEQID3
SEQID7
YLGQRDTPEWTSDPKALEVFKRFSRDLVEIESKVVGMMNHDPELKNRNGPAKFPMMLLYPN
YLGQRDTPEWTSDPKALEVFKRFSRDLVEIESKVVGMMNHDPELKNRNGPAKFPMMLLYPN

SEQID3
SEQID7
TSDHKGAAAGLTAKGIPNSISI
TSDHKGAAAGLTAKGIPNSISI

①

LOX-1 NA

Compare v (ID 5, 1)
mutant (ID 6, 2)

2311 (P5)
3574 (P7)

CLUSTAL W (1.8) multiple sequence alignment

EACH DIFFER 1 NA

63

WT
MUT
WT
MUT

SEQID5 Neruda
SEQID6 A618
SEQID1 Barke
SEQID2 D112

ATGCTGCTGGGAGGGCTGATCGACACCCTCACGGGGGCGAACAAGAGCGCCCGGCTCAAG
ATGCTGCTGGGAGGGCTGATCGACACCCTCACGGGGGCGAACAAGAGCGCCCGGCTCAAG
ATGCTGCTGGGAGGGCTGATCGACACCCTCACGGGGGCGAACAAGAGCGCCCGGCTCAAG
ATGCTGCTGGGAGGGCTGATCGACACCCTCACGGGGGCGAACAAGAGCGCCCGGCTCAAG

SEQID5 GGCACGGTGGTGCTCATGCGCAAGAACGTGCTGGACCTCAACGACTTCGGCGCCACCATC
SEQID6 GGCACGGTGGTGCTCATGCGCAAGAACGTGCTGGACCTCAACGACTTCGGCGCCACCATC
SEQID1 GGCACGGTGGTGCTCATGCGCAAGAACGTGCTGGACCTCAACGACTTCGGCGCCACCATC
SEQID2 GGCACGGTGGTGCTCATGCGCAAGAACGTGCTGGACCTCAACGACTTCGGCGCCACCATC

SEQID5 ATCGACGGCATCGGCGAGTTCTCGGCAAGGGCGTCACCTGCCAGCTTATCAGCTCCACC
SEQID6 ATCGACGGCATCGGCGAGTTCTCGGCAAGGGCGTCACCTGCCAGCTTATCAGCTCCACC
SEQID1 ATCGACGGCATCGGCGAGTTCTCGGCAAGGGCGTCACCTGCCAGCTTATCAGCTCCACC
SEQID2 ATCGACGGCATCGGCGAGTTCTCGGCAAGGGCGTCACCTGCCAGCTTATCAGCTCCACC

SEQID5 GCCGTCGACCAAGGTAATCACTACCCTCCTCCGGCCTTCTCCTCTGTTTACAAGATATAG
SEQID6 GCCGTCGACCAAGGTAATCACTACCCTCCTCCGGCCTTCTCCTCTGTTTACAAGATATAG
SEQID1 GCCGTCGACCAAGGTAATCACTACCCTCCTCCGGCCTTCTCCTCTGTTTACAAGATATAG
SEQID2 GCCGTCGACCAAGGTAATCACTACCCTCCTCCGGCCTTCTCCTCTGTTTACAAGATATAG

SEQID5 TATTTCTTTTCGTGTGGGCCGGCGGCCATGGATGGATGGATGTGTCTGGATCGGCTAAAGA
SEQID6 TATTTCTTTTCGTGTGGGCCGGCGGCCATGGATGGATGGATGTGTCTGGATCGGCTAAAGA
SEQID1 TATTTCTTTTCGTGTGGGCCGGCGGCCATGGATGGATGGATGTGTCTGGATCGGCTAAAGA
SEQID2 TATTTCTTTTCGTGTGGGCCGGCGGCCATGGATGGATGGATGTGTCTGGATCGGCTAAAGA

SEQID5 AGATAGGATAGCTAGCCCTGGCCGGTCTGCTTTTACCTGAGCATGGGCATATGCCATCGAA
SEQID6 AGATAGGATAGCTAGCCCTGGCCGGTCTGCTTTTACCTGAGCATGGGCATATGCCATCGAA
SEQID1 AGATAGGATAGCTAGCCCTGGCCGGTCTGCTTTTACCTGAGCATGGGCATATGCCATCGAA
SEQID2 AGATAGGATAGCTAGCCCTGGCCGGTCTGCTTTTACCTGAGCATGGGCATATGCCATCGAA

SEQID5 AAAAGAGACAACAGCATGCATGCATGGTGCGCGCACCAGACCACGCAGAGCACC GGATGC
SEQID6 AAAAGAGACAACAGCATGCATGCATGGTGCGCGCACCAGACCACGCAGAGCACC GGATGC
SEQID1 AAAAGAGACAACAGCATGCATGCATGGTGCGCGCACCAGACCACGCAGAGCACC GGATGC
SEQID2 AAAAGAGACAACAGCATGCATGCATGGTGCGCGCACCAGACCACGCAGAGCACC GGATGC

SEQID5 TCGAGACAAAGCAACACAACAAGCAAGGACGACACGTCAAAAGCAACACAACAAGCAAGG
SEQID6 TCGAGACAAAGCAACACAACAAGCAAGGACGACACGTCAAAAGCAACACAACAAGCAAGG
SEQID1 TCGAGACAAAGCAACACAACAAGCAAGGACGACACGTCAAAAGCAACACAACAAGCAAGG
SEQID2 TCGAGACAAAGCAACACAACAAGCAAGGACGACACGTCAAAAGCAACACAACAAGCAAGG

SEQID5 ACGGCACGTCAAAAGCAACACAACCTAAACTAAAGCACAAAGACGTAAGAGCAAGCACA
SEQID6 ACGGCACGTCAAAAGCAACACAACCTAAACTAAAGCACAAAGACGTAAGAGCAAGCACA
SEQID1 ACGGCACGTCAAAAGCAACACAACCTAAACTAAAGCACAAAGACGTAAGAGCAAGCACA
SEQID2 ACGGCACGTCAAAAGCAACACAACCTAAACTAAAGCACAAAGACGTAAGAGCAAGCACA

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SEQID5	CAATCAGCAGGCTATAAACAGTTGTCATCAAAAACAACGCTGGAAGAGAGAGAGAAGGAA
SEQID6	CAATCAGCAGGCTATAAACAGTTGTCATCAAAAACAACGCTGGAAGAGAGAGAGAAGGAA
SEQID1	CAATCAGCAGGCTATAAACAGTTGTCATCAAAAACAACGCTGGAAGAGAGAGAGAAGGAA
SEQID2	CAATCAGCAGGCTATAAACAGTTGTCATCAAAAACAACGCTGGAAGAGAGAGAGAAGGAA

SEQID5	GGAAGTAGTAGCCATGAAAAATTAAATCACCGGGCGTTGCTCTTTGCCCAACAATTAATC
SEQID6	GGAAGTAGTAGCCATGAAAAATTAAATCACCGGGCGTTGCTCTTTGCCCAACAATTAATC
SEQID1	GGAAGTAGTAGCCATGAAAAATTAAATCACCGGGCGTTGCTCTTTGCCCAACAATTAATC
SEQID2	GGAAGTAGTAGCCATGAAAAATTAAATCACCGGGCGTTGCTCTTTGCCCAACAATTAATC

SEQID5	AAGCAGGATACGTGGCATGTATAGTTCTTGTAAGTAACTAAGCATGTGATATGAGAAGG
SEQID6	AAGCAGGATACGTGGCATGTATAGTTCTTGTAAGTAACTAAGCATGTGATATGAGAAGG
SEQID1	AAGCAGGATACGTGGCATGTATAGTTCTTGTAAGTAACTAAGCATGTGATATGAGAAGG
SEQID2	AAGCAGGATACGTGGCATGTATAGTTCTTGTAAGTAACTAAGCATGTGATATGAGAAGG

SEQID5	TACGTGGTGGTGCAGACAACGGCGGTCGCGGGAAGGTGGGCGCGGAGGCGGAGCTGGAGC
SEQID6	TACGTGGTGGTGCAGACAACGGCGGTCGCGGGAAGGTGGGCGCGGAGGCGGAGCTGGAGC
SEQID1	TACGTGGTGGTGCAGACAACGGCGGTCGCGGGAAGGTGGGCGCGGAGGCGGAGCTGGAGC
SEQID2	TACGTGGTGGTGCAGACAACGGCGGTCGCGGGAAGGTGGGCGCGGAGGCGGAGCTGGAGC

SEQID5	AGTGGGTGACGAGCCTGCCGTCGCTGACGACGGGGGAGTCCAAGTTCGGCCTCACCTTCG
SEQID6	AGTGGGTGACGAGCCTGCCGTCGCTGACGACGGGGGAGTCCAAGTTCGGCCTCACCTTCG
SEQID1	AGTGGGTGACGAGCCTGCCGTCGCTGACGACGGGGGAGTCCAAGTTCGGCCTCACCTTCG
SEQID2	AGTGGGTGACGAGCCTGCCGTCGCTGACGACGGGGGAGTCCAAGTTCGGCCTCACCTTCG

SEQID5	ACTGGGAGGTGGAGAAGCTCGGGGTGCCGGGCGCCATCGTCGTCAACAACCTACCACAGCT
SEQID6	ACTGGGAGGTGGAGAAGCTCGGGGTGCCGGGCGCCATCGTCGTCAACAACCTACCACAGCT
SEQID1	ACTGGGAGGTGGAGAAGCTCGGGGTGCCGGGCGCCATCGTCGTCAACAACCTACCACAGCT
SEQID2	ACTGGGAGGTGGAGAAGCTCGGGGTGCCGGGCGCCATCGTCGTCAACAACCTACCACAGCT

SEQID5	CCGAGTTCCTGCTTAAAACCATCACCTCCACGACGTCCCCGGCCGAGCGGCAACCTCA
SEQID6	CCGAGTTCCTGCTTAAAACCATCACCTCCACGACGTCCCCGGCCGAGCGGCAACCTCA
SEQID1	CCGAGTTCCTGCTTAAAACCATCACCTCCACGACGTCCCCGGCCGAGCGGCAACCTCA
SEQID2	CCGAGTTCCTGCTTAAAACCATCACCTCCACGACGTCCCCGGCCGAGCGGCAACCTCA

SEQID5	CCTTCGTCGCCAACTCATGGATCTACCCGCGCCCAACTACCGATACAGCCGCGTCTTCT
SEQID6	CCTTCGTCGCCAACTCATGGATCTACCCGCGCCCAACTACCGATACAGCCGCGTCTTCT
SEQID1	CCTTCGTCGCCAACTCATGGATCTACCCGCGCCCAACTACCGATACAGCCGCGTCTTCT
SEQID2	CCTTCGTCGCCAACTCATGGATCTACCCGCGCCCAACTACCGATACAGCCGCGTCTTCT

SEQID5	TCGCCAACGACGTGCGTGGATTTTCCTCTACTTTCTCTCCTTTCATTTTCACCGCCTTC
SEQID6	TCGCCAACGACGTGCGTGGATTTTCCTCTACTTTCTCTCCTTTCATTTTCACCGCCTTC
SEQID1	TCGCCAACGACGTGCGTGGATTTTCCTCTACTTTCTCTCCTTTCATTTTCACCGCCTTC
SEQID2	TCGCCAACGACGTGCGTGGATTTTCCTCTACTTTCTCTCCTTTCATTTTCACCGCCTTC

SEQID5	GTCATTTCATGGTCGATCATTAAGTCTTGCCAGGACAATAGATGATGAGCTAGGAGTGGTT
SEQID6	GTCATTTCATGGTCGATCATTAAGTCTTGCCAGGACAATAGATGATGAGCTAGGAGTGGTT
SEQID1	GTCATTTCATGGTCGATCATTAAGTCTTGCCAGGACAATAGATGATGAGCTAGGAGTGGTT
SEQID2	GTCATTTCATGGTCGATCATTAAGTCTTGCCAGGACAATAGATGATGAGCTAGGAGTGGTT

SEQID5	ACCACTTAGCAGTACGTACATTATTTATTCCTGTTGGTAGAAAAGGATATGGTTTGGTG
SEQID6	ACCACTTAGCAGTACGTACATTATTTATTCCTGTTGGTAGAAAAGGATATGGTTTGGTG
SEQID1	ACCACTTAGCAGTACGTACATTATTTATTCCTGTTGGTAGAAAAGGATATGGTTTGGTG
SEQID2	ACCACTTAGCAGTACGTACATTATTTATTCCTGTTGGTAGAAAAGGATATGGTTTGGTG

SEQID5	CAGATCGACACAAGATTGAATGAAAGTTGCACCGTGGCACCCTGGCAGCGTGGTAGGTGA
SEQID6	CAGATCGACACAAGATTGAATGAAAGTTGCACCGTGGCACCCTGGCAGCGTGGTAGGTGA
SEQID1	CAGATCGACACAAGATTGAATGAAAGTTGCACCGTGGCACCCTGGCAGCGTGGTAGGTGA
SEQID2	CAGATCGACACAAGATTGAATGAAAGTTGCACCGTGGCACCCTGGCAGCGTGGTAGGTGA

SEQID5	AAATAACTGTTGCACGGATCCACCCACATGATTGTTTTTCATGAATAAACTTTTTAAGGAT
SEQID6	AAATAACTGTTGCACGGATCCACCCACATGATTGTTTTTCATGAATAAACTTTTTAAGGAT
SEQID1	AAATAACTGTTGCACGGATCCACCCACATGATTGTTTTTCATGAATAAACTTTTTAAGGAT
SEQID2	AAATAACTGTTGCACGGATCCACCCACATGATTGTTTTTCATGAATAAACTTTTTAAGGAT

SEQID5	GTGTCTAGCCACATCTAGATGCATGTCACATAATTATTGCATACCAAACGATTAAATTA
SEQID6	GTGTCTAGCCACATCTAGATGCATGTCACATAATTATTGCATACCAAACGATTAAATTA
SEQID1	GTGTCTAGCCACATCTAGATGCATGTCACATAATTATTGCATACCAAACGATTAAATTA
SEQID2	GTGTCTAGCCACATCTAGATGCATGTCACATAATTATTGCATACCAAACGATTAAATTA

SEQID5	AGCATAAAAAGAAAAGGAAAAAAATACTCACATATCTCGACGTAAGATCAATGATATAGT
SEQID6	AGCATAAAAAGAAAAGGAAAAAAATACTCACATATCTCGACGTAAGATCAATGATATAGT
SEQID1	AGCATAAAAAGAAAAGGAAAAAAATACTCACATATCTCGACGTAAGATCAATGATATAGT
SEQID2	AGCATAAAAAGAAAAGGAAAAAAATACTCACATATCTCGACGTAAGATCAATGATATAGT

SEQID5	ATTTAGATATGCAATATTTATCTTACATCTAAACCTTTCTTCATTCTTAAATATAAGACA
SEQID6	ATTTAGATATGCAATATTTATCTTACATCTAAACCTTTCTTCATTCTTAAATATAAGACA
SEQID1	ATTTAGATATGCAATATTTATCTTACATCTAAACCTTTCTTCATTCTTAAATATAAGACA
SEQID2	ATTTAGATATGCAATATTTATCTTACATCTAAACCTTTCTTCATTCTTAAATATAAGACA

SEQID5	TTTGTAAGATTTCACTATGGACAACATACGAAACAAAATCAGTGGATCTCTCTATGCATT
SEQID6	TTTGTAAGATTTCACTATGGACAACATACGAAACAAAATCAGTGGATCTCTCTATGCATT
SEQID1	TTTGTAAGATTTCACTATGGACAACATACGAAACAAAATCAGTGGATCTCTCTATGCATT
SEQID2	TTTGTAAGATTTCACTATGGACAACATACGAAACAAAATCAGTGGATCTCTCTATGCATT

SEQID5	CATTATGTAGTCTATAATAAAATCTTTAAAAGATCGTATATTTTGCAACGGAGGGAGTAA
SEQID6	CATTATGTAGTCTATAATAAAATCTTTAAAAGATCGTATATTTTGCAACGGAGGGAGTAA
SEQID1	CATTATGTAGTCTATAATAAAATCTTTAAAAGATCGTATATTTTGCAACGGAGGGAGTAA
SEQID2	CATTATGTAGTCTATAATAAAATCTTTAAAAGATCGTATATTTTGCAACGGAGGGAGTAA

SEQID5	AACATAACTTTTTAATAGTAATGTTGCACGGCTCCACACTCGCAGACGTACCTGCCGAGC
SEQID6	AACATAACTTTTTAATAGTAATGTTGCACGGCTCCACACTCGCAGACGTACCTGCCGAGC
SEQID1	AACATAACTTTTTAATAGTAATGTTGCACGGCTCCACACTCGCAGACGTACCTGCCGAGC
SEQID2	AACATAACTTTTTAATAGTAATGTTGCACGGCTCCACACTCGCAGACGTACCTGCCGAGC

SEQID5	CAGATGCCGGCGGCGCTGAAGCCGTACCGCGACGACGAGCTCCGGAACCTGCGTGGCGAC
SEQID6	CAGATGCCGGCGGCGCTGAAGCCGTACCGCGACGACGAGCTCCGGAACCTGCGTGGCGAC
SEQID1	CAGATGCCGGCGGCGCTGAAGCCGTACCGCGACGACGAGCTCCGGAACCTGCGTGGCGAC
SEQID2	CAGATGCCGGCGGCGCTGAAGCCGTACCGCGACGACGAGCTCCGGAACCTGCGTGGCGAC

SEQID5	GACCAGCAGGGCCCGTACCAGGAGCACGACCGCATCTACCGCTACGACGTCTACAACGAC
SEQID6	GACCAGCAGGGCCCGTACCAGGAGCACGACCGCATCTACCGCTACGACGTCTACAACGAC
SEQID1	GACCAGCAGGGCCCGTACCAGGAGCACGACCGCATCTACCGCTACGACGTCTACAACGAC
SEQID2	GACCAGCAGGGCCCGTACCAGGAGCACGACCGCATCTACCGCTACGACGTCTACAACGAC

SEQID5	CTCGGCGAGGGCCGCCCCATCCTCGGCGGCAACTCCGACCACCCCTTACCCGCGCCGCGGC
SEQID6	CTCGGCGAGGGCCGCCCCATCCTCGGCGGCAACTCCGACCACCCCTTACCCGCGCCGCGGC
SEQID1	CTCGGCGAGGGCCGCCCCATCCTCGGCGGCAACTCCGACCACCCCTTACCCGCGCCGCGGC
SEQID2	CTCGGCGAGGGCCGCCCCATCCTCGGCGGCAACTCCGACCACCCCTTACCCGCGCCGCGGC

SEQID5	CGCACGGAGCGCAAGCCCCAAGCCAGCGACCCGAGCCTGGAGAGCCGGCTGTGCTGCTG
SEQID6	CGCACGGAGCGCAAGCCCCAAGCCAGCGACCCGAGCCTGGAGAGCCGGCTGTGCTGCTG
SEQID1	CGCACGGAGCGCAAGCCCCAAGCCAGCGACCCGAGCCTGGAGAGCCGGCTGTGCTGCTG
SEQID2	CGCACGGAGCGCAAGCCCCAAGCCAGCGACCCGAGCCTGGAGAGCCGGCTGTGCTGCTG

SEQID5	GAGCAGATCTACGTGCCGCGGGACGAGAAGTTCGGCCACCTCAAGACGTCCGACTTCCTG
SEQID6	GAGCAGATCTACGTGCCGCGGGACGAGAAGTTCGGCCACCTCAAGACGTCCGACTTCCTG
SEQID1	GAGCAGATCTACGTGCCGCGGGACGAGAAGTTCGGCCACCTCAAGACGTCCGACTTCCTG
SEQID2	GAGCAGATCTACGTGCCGCGGGACGAGAAGTTCGGCCACCTCAAGACGTCCGACTTCCTG

SEQID5	GGCTACTCCATCAAGGCCATCACGCAGGGCATCCTGCCGGCCGTGCGCACCTACGTGGAC
SEQID6	GGCTACTCCATCAAGGCCATCACGCAGGGCATCCTGCCGGCCGTGCGCACCTACGTGGAC
SEQID1	GGCTACTCCATCAAGGCCATCACGCAGGGCATCCTGCCGGCCGTGCGCACCTACGTGGAC
SEQID2	GGCTACTCCATCAAGGCCATCACGCAGGGCATCCTGCCGGCCGTGCGCACCTACGTGGAC

SEQID5	ACCACCCCGGCGAGTTGCACTCCTTCCAGGACATCATCAACCTCTATGAGGGCGGCATC
SEQID6	ACCACCCCGGCGAGTTGCACTCCTTCCAGGACATCATCAACCTCTATGAGGGCGGCATC
SEQID1	ACCACCCCGGCGAGTTGCACTCCTTCCAGGACATCATCAACCTCTATGAGGGCGGCATC
SEQID2	ACCACCCCGGCGAGTTGCACTCCTTCCAGGACATCATCAACCTCTATGAGGGCGGCATC

SEQID5	AAGCTGCCCAAGGTGGCCGCCCTGGAGGAGCTCCGTAAGCAGTTCCTCGCTCCAGCTCATC
SEQID6	AAGCTGCCCAAGGTGGCCGCCCTGGAGGAGCTCCGTAAGCAGTTCCTCGCTCCAGCTCATC
SEQID1	AAGCTGCCCAAGGTGGCCGCCCTGGAGGAGCTCCGTAAGCAGTTCCTCGCTCCAGCTCATC
SEQID2	AAGCTGCCCAAGGTGGCCGCCCTGGAGGAGCTCCGTAAGCAGTTCCTCGCTCCAGCTCATC

2160

SEQID5 AAGGACCTCCTCCCCGTCGGCGGCGACTCCCTGCTTAAGCTCCCCGTGCCCCACATCATC
SEQID6 AAGGACCTCCTCCCCGTCGGCGGCGACTCCCTGCTTAAGCTCCCCGTGCCCCACATCATC
SEQID1 AAGGACCTCCTCCCCGTCGGCGGCGACTCCCTGCTTAAGCTCCCCGTGCCCCACATCATC
SEQID2 AAGGACCTCCTCCCCGTCGGCGGCGACTCCCTGCTTAAGCTCCCCGTGCCCCACATCATC

2220

SEQID5 CAGGAGAACAAGCAGGCGTGGAGGACCGACGAGGAGTTCGCACGGGAGGTGCTCGCCGGC
SEQID6 CAGGAGAACAAGCAGGCGTGGAGGACCGACGAGGAGTTCGCACGGGAGGTGCTCGCCGGC
SEQID1 CAGGAGAACAAGCAGGCGTGGAGGACCGACGAGGAGTTCGCACGGGAGGTGCTCGCCGGC
SEQID2 CAGGAGAACAAGCAGGCGTGGAGGACCGACGAGGAGTTCGCACGGGAGGTGCTCGCCGGC

2280

SEQID5 GTCAACCCGGTCATGATCACGCGTCTCACGGT²³GAGTCAGCGATTATTTGTTTCATTGTGTG
SEQID6 GTCAACCCGGTCATGATCACGCGTCTCACGATGAGTCAGCGATTATTTGTTTCATTGTGTG
SEQID1 GTCAACCCGGTCATGATCACGCGTCTCACGGT²³GAGTCAGCGATTATTTGTTTCATTGTGTG
SEQID2 GTCAACCCGGTCATGATCACGCGTCTCACGGT²³GAGTCAGCGATTATTTGTTTCATTGTGTG

2311

SEQID5 TGTATGGTGTCCATGGTGAGAAAGTGCAGATCTTGATTGCGTTGGGTGCGATGCACGCA
SEQID6 TGTATGGTGTCCATGGTGAGAAAGTGCAGATCTTGATTGCGTTGGGTGCGATGCACGCA
SEQID1 TGTATGGTGTCCATGGTGAGAAAGTGCAGATCTTGATTGCGTTGGGTGCGATGCACGCA
SEQID2 TGTATGGTGTCCATGGTGAGAAAGTGCAGATCTTGATTGCGTTGGGTGCGATGCACGCA

SEQID5 TGCTGCATGCATGCAGGAGTTC²³CGCCAAAAAGTAGTCTGGACCCTAGCAAGTTTGGTGA
SEQID6 TGCTGCATGCATGCAGGAGTTC²³CGCCAAAAAGTAGTCTGGACCCTAGCAAGTTTGGTGA
SEQID1 TGCTGCATGCATGCAGGAGTTC²³CGCCAAAAAGTAGTCTGGACCCTAGCAAGTTTGGTGA
SEQID2 TGCTGCATGCATGCAGGAGTTC²³CGCCAAAAAGTAGTCTGGACCCTAGCAAGTTTGGTGA

SEQID5 CCACACCAGCACCATCACGGCGGAGCACATAGAGAAGAACCTCGAGGGCCTCACGGTGCA
SEQID6 CCACACCAGCACCATCACGGCGGAGCACATAGAGAAGAACCTCGAGGGCCTCACGGTGCA
SEQID1 CCACACCAGCACCATCACGGCGGAGCACATAGAGAAGAACCTCGAGGGCCTCACGGTGCA
SEQID2 CCACACCAGCACCATCACGGCGGAGCACATAGAGAAGAACCTCGAGGGCCTCACGGTGCA

SEQID5 GCAGGTAATTGGTCCAAGCCATCGACATCAACTATGATTTACCTAGGAGTAATTGGTAGC
SEQID6 GCAGGTAATTGGTCCAAGCCATCGACATCAACTATGATTTACCTAGGAGTAATTGGTAGC
SEQID1 GCAGGTAATTGGTCCAAGCCATCGACATCAACTATGATTTACCTAGGAGTAATTGGTAGC
SEQID2 GCAGGTAATTGGTCCAAGCCATCGACATCAACTATGATTTACCTAGGAGTAATTGGTAGC

SEQID5 TGTAGATAATTTGGCTTCGTTGCAATTAATTTGATGCTGGCCGATCAAGTGATCGTATTG
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SEQID1 TGTAGATAATTTGGCTTCGTTGCAATTAATTTGATGCTGGCCGATCAAGTGATCGTATTG
SEQID2 TGTAGATAATTTGGCTTCGTTGCAATTAATTTGATGCTGGCCGATCAAGTGATCGTATTG

SEQID5 GGT²³TTGAAATTTGCAGGCGCTGGAAAGCAACAGGCTGTACATCCTTGATCACCATGACCG
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SEQID1 GGT²³TTGAAATTTGCAGGCGCTGGAAAGCAACAGGCTGTACATCCTTGATCACCATGACCG
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SEQID5 GCCCATCATCCAGGGCGGCCTTACCACGGCCAAGAGCAAGGTTTACACGCCGGTGCCAG
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SEQID1 GCCCATCATCCAGGGCGGCCTTACCACGGCCAAGAGCAAGGTTTACACGCCGGTGCCAG
SEQID2 GCCCATCATCCAGGGCGGCCTTACCACGGCCAAGAGCAAGGTTTACACGCCGGTGCCAG

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SEQID6 CGGCTCCGTCTGAAGGCTGGGTGTGGGAGCTCGCCAAGGCCTACGTGCGCGTCAATGACTC
SEQID1 CGGCTCCGTCTGAAGGCTGGGTGTGGGAGCTCGCCAAGGCCTACGTGCGCGTCAATGACTC
SEQID2 CGGCTCCGTCTGAAGGCTGGGTGTGGGAGCTCGCCAAGGCCTACGTGCGCGTCAATGACTC

SEQID5 CGGGTGGCACCAGCTCGTCAGCCACTGGTACGTTCTCCACGGTCGATGTGATTCACTCAG
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SEQID1 CGGGTGGCACCAGCTCGTCAGCCACTGGTACGTTCTCCACGGTCGATGTGATTCACTCAG
SEQID2 CGGGTGGCACCAGCTCGTCAGCCACTGGTACGTTCTCCACGGTCGATGTGATTCACTCAG

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SEQID6 TCGATGCACAACAACCTGATCGAAATATGATTGATTGAAACGCGCAGGCTGAACACTCACG
SEQID1 TCGATGCACAACAACCTGATCGAAATATGATTGATTGAAACGCGCAGGCTGAACACTCACG
SEQID2 TCGATGCACAACAACCTGATCGAAATATGATTGATTGAAACGCGCAGGCTGAACACTCACG

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SEQID6 CGGTGATGGAGCCGTTTCGTGATCTCGACGAACCGGCACCTTAGCGTGACGCACCCGGTGC
SEQID1 CGGTGATGGAGCCGTTTCGTGATCTCGACGAACCGGCACCTTAGCGTGACGCACCCGGTGC
SEQID2 CGGTGATGGAGCCGTTTCGTGATCTCGACGAACCGGCACCTTAGCGTGACGCACCCGGTGC

SEQID5 ACAAGCTGCTGAGCCCGCACTACCGCGACACCATGACCATCAACGCGCTGGCGCGGCAGA
SEQID6 ACAAGCTGCTGAGCCCGCACTACCGCGACACCATGACCATCAACGCGCTGGCGCGGCAGA
SEQID1 ACAAGCTGCTGAGCCCGCACTACCGCGACACCATGACCATCAACGCGCTGGCGCGGCAGA
SEQID2 ACAAGCTGCTGAGCCCGCACTACCGCGACACCATGACCATCAACGCGCTGGCGCGGCAGA

SEQID5 CGCTCATCAACGCCGGCGGCATCTTCGAGATGACGGTGTTCGCCGGCAAGTTCGCGTTGG 3240
SEQID6 CGCTCATCAACGCCGGCGGCATCTTCGAGATGACGGTGTTCGCCGGCAAGTTCGCGTTGG
SEQID1 CGCTCATCAACGCCGGCGGCATCTTCGAGATGACGGTGTTCGCCGGCAAGTTCGCGTTGG
SEQID2 CGCTCATCAACGCCGGCGGCATCTTCGAGATGACGGTGTTCGCCGGCAAGTTCGCGTTGG

SEQID5 GGATGTCGGCCGTGGTGTACAAGGACTGGAAGTTCACCGAGCAGGGACTGCCGGACGATC
SEQID6 GGATGTCGGCCGTGGTGTACAAGGACTGGAAGTTCACCGAGCAGGGACTGCCGGACGATC
SEQID1 GGATGTCGGCCGTGGTGTACAAGGACTGGAAGTTCACCGAGCAGGGACTGCCGGACGATC
SEQID2 GGATGTCGGCCGTGGTGTACAAGGACTGGAAGTTCACCGAGCAGGGACTGCCGGACGATC

SEQID5 TCATCAAGAGGTACGTACCTGGTAAATGTTATGAATGTGTAAAAACAAATTGGGCGTCTCG
SEQID6 TCATCAAGAGGTACGTACCTGGTAAATGTTATGAATGTGTAAAAACAAATTGGGCGTCTCG
SEQID1 TCATCAAGAGGTACGTACCTGGTAAATGTTATGAATGTGTAAAAACAAATTGGGCGTCTCG
SEQID2 TCATCAAGAGGTACGTACCTGGTAAATGTTATGAATGTGTAAAAACAAATTGGGCGTCTCG

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SEQID6 CTCACTGACAGGAACGTGGTAAAAAATGCAGGGGCATGGCGGTGGAGGACCCGTCGAG
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SEQID2 CTCACTGACAGGAACGTGGTAAAAAATGCAGGGGCATGGCGGTGGAGGACCCGTCGAG

SEQID5 CCCGTACAAGGTGCGGTTGCTGGTGTCTGGACTACCCGTACGCGGCGGACGGGCTGGCGAT
SEQID6 CCCGTACAAGGTGCGGTTGCTGGTGTCTGGACTACCCGTACGCGGCGGACGGGCTGGCGAT
SEQID1 CCCGTACAAGGTGCGGTTGCTGGTGTCTGGACTACCCGTACGCGGCGGACGGGCTGGCGAT
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SEQID5 CTGGCAGCCATTGAGCAGTACGTGAGCGAGTACCTGGCCATCTACTACCCGAACGACGG
SEQID6 CTGGCAGCCATTGAGCAGTACGTGAGCGAGTACCTGGCCATCTACTACCCGAACGACGG
SEQID1 CTGGCAGCCATTGAGCAGTACGTGAGCGAGTACCTGGCCATCTACTACCCGAACGACGG
SEQID2 CTGGCAGCCATTGAGCAGTACGTGAGCGAGTACCTGGCCATCTACTACCCGAACGACGG

SEQID5 CGTGCTGCAGGGCGATACGGAGGTGCAGGCGTGGTGAAGGAGACGCGCGAGGTGCGGCA
SEQID6 CGTGCTGCAGGGCGATACGGAGGTGCAGGCGTGGTGAAGGAGACGCGCGAGGTGCGGCA
SEQID1 CGTGCTGCAGGGCGATACGGAGGTGCAGGCGTGGTGAAGGAGACGCGCGAGGTGCGGCA
SEQID2 CGTGCTGCAGGGCGATACGGAGGTGCAGGCGTGGTGAAGGAGACGCGCGAGGTGCGGCA

D112

3574

SEQID5 CGGCGACCTCAAGGACGCCCCATGGTGGCCCAAGATGCAAAGTGTGCCGGAGCTGGCCAA
SEQID6 CGGCGACCTCAAGGACGCCCCATGGTGGCCCAAGATGCAAAGTGTGCCGGAGCTGGCCAA
SEQID1 CGGCGACCTCAAGGACGCCCCATGGTGGCCCAAGATGCAAAGTGTGCCGGAGCTGGCCAA
SEQID2 CGGCGACCTCAAGGACGCCCCATGGTGGCCCAAGATGCAAAGTGTGCCGGAGCTGGCCAA

SEQID5 GGCGTGCAACCACCATCATCTGGATCGGGTCGGCGCTGCATGCGGCAGTCAACTTCGGGCA
SEQID6 GGCGTGCAACCACCATCATCTGGATCGGGTCGGCGCTGCATGCGGCAGTCAACTTCGGGCA
SEQID1 GGCGTGCAACCACCATCATCTGGATCGGGTCGGCGCTGCATGCGGCAGTCAACTTCGGGCA
SEQID2 GGCGTGCAACCACCATCATCTGGATCGGGTCGGCGCTGCATGCGGCAGTCAACTTCGGGCA

SEQID5 GTACCCCTACGCGGGGTTCTCCCGAACCGGCCGACGGTGAGCCGGCGCCGCATGCCGGA
SEQID6 GTACCCCTACGCGGGGTTCTCCCGAACCGGCCGACGGTGAGCCGGCGCCGCATGCCGGA
SEQID1 GTACCCCTACGCGGGGTTCTCCCGAACCGGCCGACGGTGAGCCGGCGCCGCATGCCGGA
SEQID2 GTACCCCTACGCGGGGTTCTCCCGAACCGGCCGACGGTGAGCCGGCGCCGCATGCCGGA

SEQID5	GCCCCGGCACGGAGGAGTACGCGGAGCTGGAGCGCGACCCGGAGCGGGCCTTCATCCACAC
SEQID6	GCCCCGGCACGGAGGAGTACGCGGAGCTGGAGCGCGACCCGGAGCGGGCCTTCATCCACAC
SEQID1	GCCCCGGCACGGAGGAGTACGCGGAGCTGGAGCGCGACCCGGAGCGGGCCTTCATCCACAC
SEQID2	GCCCCGGCACGGAGGAGTACGCGGAGCTGGAGCGCGACCCGGAGCGGGCCTTCATCCACAC

SEQID5	CATCACGAGCCAGATCCAGACCATCATCGGCGTGTCGCTGCTGGAGGTGCTGTCGAAGCA
SEQID6	CATCACGAGCCAGATCCAGACCATCATCGGCGTGTCGCTGCTGGAGGTGCTGTCGAAGCA
SEQID1	CATCACGAGCCAGATCCAGACCATCATCGGCGTGTCGCTGCTGGAGGTGCTGTCGAAGCA
SEQID2	CATCACGAGCCAGATCCAGACCATCATCGGCGTGTCGCTGCTGGAGGTGCTGTCGAAGCA

SEQID5	CTCCTCCGACGAGCTGTACCTCGGGCAGCGGGACACGCCGGAGTGGACCTCGGACCCAAA
SEQID6	CTCCTCCGACGAGCTGTACCTCGGGCAGCGGGACACGCCGGAGTGGACCTCGGACCCAAA
SEQID1	CTCCTCCGACGAGCTGTACCTCGGGCAGCGGGACACGCCGGAGTGGACCTCGGACCCAAA
SEQID2	CTCCTCCGACGAGCTGTACCTCGGGCAGCGGGACACGCCGGAGTGGACCTCGGACCCAAA

SEQID5	GGCCCTGGAGGTGTTCAAGCGGTTTCAGCGACCGGCTGGTGGAGATCGAGAGCAAGGTGGT
SEQID6	GGCCCTGGAGGTGTTCAAGCGGTTTCAGCGACCGGCTGGTGGAGATCGAGAGCAAGGTGGT
SEQID1	GGCCCTGGAGGTGTTCAAGCGGTTTCAGCGACCGGCTGGTGGAGATCGAGAGCAAGGTGGT
SEQID2	GGCCCTGGAGGTGTTCAAGCGGTTTCAGCGACCGGCTGGTGGAGATCGAGAGCAAGGTGGT

SEQID5	GGGCATGAACCATGACCCGGAGCTCAAGAACCGCAACGGCCCCGGCTAAGTTTCCCTACAT
SEQID6	GGGCATGAACCATGACCCGGAGCTCAAGAACCGCAACGGCCCCGGCTAAGTTTCCCTACAT
SEQID1	GGGCATGAACCATGACCCGGAGCTCAAGAACCGCAACGGCCCCGGCTAAGTTTCCCTACAT
SEQID2	GGGCATGAACCATGACCCGGAGCTCAAGAACCGCAACGGCCCCGGCTAAGTTTCCCTACAT

SEQID5	GCTGCTCTACCCCAACACCTCCGACCACAAGGGCGCCGCTGCCGGGCTTACCGCCAAGGG
SEQID6	GCTGCTCTACCCCAACACCTCCGACCACAAGGGCGCCGCTGCCGGGCTTACCGCCAAGGG
SEQID1	GCTGCTCTACCCCAACACCTCCGACCACAAGGGCGCCGCTGCCGGGCTTACCGCCAAGGG
SEQID2	GCTGCTCTACCCCAACACCTCCGACCACAAGGGCGCCGCTGCCGGGCTTACCGCCAAGGG

SEQID5	CATCCCCAACAGCATCTCCATCTAA
SEQID6	CATCCCCAACAGCATCTCCATCTAA
SEQID1	CATCCCCAACAGCATCTCCATCTAA
SEQID2	CATCCCCAACAGCATCTCCATCTAA

LOX-1 Protein

Compare WT/MUTANTS

CLUSTAL W (1.8) multiple sequence alignment

ClBarke cv. Neruda	SEQID3 WT	MLLGGLIDTLTGANKSARLKGTVVLMRKNVLDLNDFGATIIDGIGEFGLGKGVTCQLISST	60
	SEQID4 MUTD112	MLLGGLIDTLTGANKSARLKGTVVLMRKNVLDLNDFGATIIDGIGEFGLGKGVTCQLISST	
	SEQID7 WT	MLLGGLIDTLTGANKSARLKGTVVLMRKNVLDLNDFGATIIDGIGEFGLGKGVTCQLISST	
	SEQID8 MUT A618	MLLGGLIDTLTGANKSARLKGTVVLMRKNVLDLNDFGATIIDGIGEFGLGKGVTCQLISST *****	
	SEQID3	AVDQDNGGRGKVGAEAELEQWVTSLSPLTTGESKFGLTFDWEVEKLGVPGAIVVNNYHSS	120
	SEQID4	AVDQDNGGRGKVGAEAELEQWVTSLSPLTTGESKFGLTFDWEVEKLGVPGAIVVNNYHSS	
	SEQID7	AVDQDNGGRGKVGAEAELEQWVTSLSPLTTGESKFGLTFDWEVEKLGVPGAIVVNNYHSS	
	SEQID8	AVDQDNGGRGKVGAEAELEQWVTSLSPLTTGESKFGLTFDWEVEKLGVPGAIVVNNYHSS *****	
	SEQID3	EFLCLKTITLHDPGRSGNLTFFVANSWIYPAANYRYSRVFFANDTYLPSQMPAALKPYRDD	180
	SEQID4	EFLCLKTITLHDPGRSGNLTFFVANSWIYPAANYRYSRVFFANDTYLPSQMPAALKPYRDD	
	SEQID7	EFLCLKTITLHDPGRSGNLTFFVANSWIYPAANYRYSRVFFANDTYLPSQMPAALKPYRDD	
	SEQID8	EFLCLKTITLHDPGRSGNLTFFVANSWIYPAANYRYSRVFFANDTYLPSQMPAALKPYRDD *****	
	SEQID3	ELRNLRGDDQQGPYQEHDRYRYDVYNDLGEGRPILGGNSDHPYPRRGRTERKPNASDPS	240
	SEQID4	ELRNLRGDDQQGPYQEHDRYRYDVYNDLGEGRPILGGNSDHPYPRRGRTERKPNASDPS	
	SEQID7	ELRNLRGDDQQGPYQEHDRYRYDVYNDLGEGRPILGGNSDHPYPRRGRTERKPNASDPS	
	SEQID8	ELRNLRGDDQQGPYQEHDRYRYDVYNDLGEGRPILGGNSDHPYPRRGRTERKPNASDPS *****	
	SEQID3	LESRLSLLEQIYVPRDEKFGHLKTSDFLGYSIKAITQGILPAVRTYVDTTTPEGFDSFQDI	300
	SEQID4	LESRLSLLEQIYVPRDEKFGHLKTSDFLGYSIKAITQGILPAVRTYVDTTTPEGFDSFQDI	
	SEQID7	LESRLSLLEQIYVPRDEKFGHLKTSDFLGYSIKAITQGILPAVRTYVDTTTPEGFDSFQDI	
	SEQID8	LESRLSLLEQIYVPRDEKFGHLKTSDFLGYSIKAITQGILPAVRTYVDTTTPEGFDSFQDI *****	
	SEQID3	INLYEGGIKLPKVAALEELRKQFPLQLIKDLLPVGGDSLLKLPVPHIIQENKQAWRTDEE	360
	SEQID4	INLYEGGIKLPKVAALEELRKQFPLQLIKDLLPVGGDSLLKLPVPHIIQENKQAWRTDEE	
	SEQID7	INLYEGGIKLPKVAALEELRKQFPLQLIKDLLPVGGDSLLKLPVPHIIQENKQAWRTDEE	
	SEQID8	INLYEGGIKLPKVAALEELRKQFPLQLIKDLLPVGGDSLLKLPVPHIIQENKQAWRTDEE *****	
	SEQID3	FAREVLAVGNPVMITRLTEFPPKSSLDPSKFGDHTSTITAHEIEKNLEGLTVQQALESNR	420
	SEQID4	FAREVLAVGNPVMITRLTEFPPKSSLDPSKFGDHTSTITAHEIEKNLEGLTVQQALESNR	
	SEQID7	FAREVLAVGNPVMITRLTEFPPKSSLDPSKFGDHTSTITAHEIEKNLEGLTVQQALESNR	
	SEQID8	FAREVLAVGNPVMITR-----L-----TMS----- ***** 376 377 378	
	SEQID3	LYILDHHDRFMPFLIDVNNLPGNFIYATRTLFFLRGDGRLTPLAIELSEPIIQGGLTTAK	480
	SEQID4	LYILDHHDRFMPFLIDVNNLPGNFIYATRTLFFLRGDGRLTPLAIELSEPIIQGGLTTAK	
	SEQID7	LYILDHHDRFMPFLIDVNNLPGNFIYATRTLFFLRGDGRLTPLAIELSEPIIQGGLTTAK	
	SEQID8	-----QRL--FVHCVCVMVS--MVRKCRS----- *: *: * .: .: *:	
	SEQID3	SKVYTPVPSGSVEGWVWELAKAYVAVNDSGWHQLVSHWLNTHAVMEPFVISTNRHLSVTH	540
	SEQID4	SKVYTPVPSGSVEGWVWELAKAYVAVNDSGWHQLVSHWLNTHAVMEPFVISTNRHLSVTH	
	SEQID7	SKVYTPVPSGSVEGWVWELAKAYVAVNDSGWHQLVSHWLNTHAVMEPFVISTNRHLSVTH	
	SEQID8	-----	

Mutant A618 = splice variant / truncation of LOX-1
at 378 (3)

SEQID3 PVHKLLSPHYRDTMTINALARQTLINAGGIFEMTVFPGKFALGMSAVVYKDWKFTEQGLP 660
 SEQID4 PVHKLLSPHYRDTMTINALARQTLINAGGIFEMTVFPGKFALGMSAVVYKDWKFTEQGLP
 SEQID7 PVHKLLSPHYRDTMTINALARQTLINAGGIFEMTVFPGKFALGMSAVVYKDWKFTEQGLP
 SEQID8 -----

SEQID3 DDLIKRGMAVEDPSSPYKVRLLVSDYPYAADGLAIWHAIEQYVSEYLAIYYPNDGVLQGD 660
 SEQID4 DDLIKRGMAVEDPSSPYKVRLLVSDYPYAADGLAIWHAIEQYVSEYLAIYYPNDGVLQGD
 SEQID7 DDLIKRGMAVEDPSSPYKVRLLVSDYPYAADGLAIWHAIEQYVSEYLAIYYPNDGVLQGD
 SEQID8 -----

SEQID3 TEVQAWWKETREVGHGDLKDAPWWPKMQSVPELAKACTTIIWIGSALHAAVNFGQYPYAG 720
 SEQID4 TEVQA-----
 SEQID7 TEVQAWWKETREVGHGDLKDAPWWPKMQSVPELAKACTTIIWIGSALHAAVNFGQYPYAG
 SEQID8 -----

SEQID3 FLPNRPTVSRRRMPEPGTEEYAELEERDPERAFIHTTITSQIQTIIGVSLLEVLSKHSSDEL 780
 SEQID4 -----
 SEQID7 FLPNRPTVSRRRMPEPGTEEYAELEERDPERAFIHTTITSQIQTIIGVSLLEVLSKHSSDEL
 SEQID8 -----

SEQID3 YLGQRDTPewTSDPKALEVFKRFSdRLVEIESKVVGmNHDPELKNRNGPAKFPYmLLYPN 840
 SEQID4 -----
 SEQID7 YLGQRDTPewTSDPKALEVFKRFSdRLVEIESKVVGmNHDPELKNRNGPAKFPYmLLYPN
 SEQID8 -----

862
 SEQID3 TSDHKGAAAGLTAKGIPNSISI
 SEQID4 -----
 SEQID7 TSDHKGAAAGLTAKGIPNSISI
 SEQID8 -----

Mutant D112 - truncated at 665

